

### **REMARKS**

Reconsideration and allowance are respectfully requested.

Claims 12-17 are now pending, with Claim 12 being the sole independent claim. Claims 18-19 have been cancelled without prejudice to or disclaimer of the subject matter recited therein. Claims 12-17 have been amended. No new matter has been added.

Applicants have filed simultaneously herewith replacement drawings to amend the view numbers to refer to Figures 1A and 1B. The corrections to the view numbers necessitate amending the Brief Description of Drawings and Examples in the specification to refer to these new view numbers. In addition, Figures 1A and 1B have had their font size increased and orientation changed to landscape.

The specification has been amended to include an abstract on a separate sheet. No new matter has been added.

Turning now to the Office Action mailed December 30, 2002:

As an initial matter, with respect to now cancelled claims 18-19, all of the Section 112, 2d paragraph, Section 101, Section 112, 1<sup>st</sup> paragraph, and Section 102(b) rejections have been rendered moot.

Regarding the question about the Sequence Listing and the region of SEQ ID NO:3 that encodes SEQ ID NO:4, the total length of the isolated cDNA consists of 1217 bp (SEQ ID NO:3) and is believed to contain a single open reading frame of 1028 bp (from 2-1030) encoding a functionally complete protein of 343 amino acids (SEQ ID NO:4). Applicants note that there is an ATG codon at position 137 of SEQ ID NO:4 (although Applicants do not believe this to be a start methionine). The termination codon is localized at position 1032 (TAG). In addition, the 3' end includes a poly(A)<sup>+</sup> tail.

Regarding the objection to the specification, Applicants have deleted all Internet hyperlinks in the specification as requested.

Regarding the Section 112, 2d paragraph rejections:

1. Claim 12 has been amended to recite "adenosine 5'-phosphosulfate". Applicants note that the interpretation of the "Clustal method of alignment" as using the default parameters set forth on page 5, lines 5-7 is correct.
2. Claim 12(b) has been amended to recite "full-length" complement, as suggested.
3. Claims reciting "a chimeric gene" have been amended to "a recombinant DNA construct", as suggested.
4. Claims 13-17 have been amended to correct their dependency.

Applicants submit that these amendments have obviated the reasons for the Examiner's rejection of claims 12-17 under Section 112, 2d paragraph.

Regarding the Section 101 (utility) rejection, Applicants respectfully traverse.

As an initial matter, Applicants submit that SEQ ID NO:3 is not an EST sequence as stated at the bottom of page 4 of the Office Action. As stated above, Applicants believe SEQ ID NO:3 to contain a single open reading frame of 1028 bp (from 2-1030) encoding a functionally complete protein of 343 amino acids (SEQ ID NO:4).

Applicants believe the following references to be representative of the knowledge of one of ordinary skill in the art:

Deyrup et al. (*The Journal of Biological Chemistry* 273 (16):9450-9456 (April 17, 1998) ("Deyrup")  
Satishchandran et al. (*Biochemistry* 31:11684-11688 (1992) ("Satishchandran")  
Arz et al. (*Biochimica et Biophysica Acta* 1218:447-452 (1994) ("Arz")  
MacRae et al. (*Biochemistry* 39:1613-1621 (2000) ("MacRae")<sup>1</sup>

Each of these references, except Arz (previously cited), are cited in a Supplemental IDS filed simultaneously herewith.

Deyrup identifies the active site P-loop as a common structural feature of APS kinase activity. See also Figure 2 in Satishchandran and Figure 1 in Arz, and Figure 2 in MacRae. Furthermore, Satishchandran (Figure 2), Arz (page 449), and MacRae (Figure 2) also disclose the (P)APS binding region.

Appendix A, attached hereto, is a Clustal V alignment of SEQ ID NO:4 of the instant claims and the following three APS kinase proteins:

1. *Catharanthus roseus* APS kinase (SEQ ID NO:13 of the instant specification; GI 2832300).
2. *Arabidopsis thaliana* APS kinase (SEQ ID NO:14 of the instant specification (GI 1076283) and also found in Figure 2 of MacRae starting at amino acid 58).<sup>2</sup>
3. *Saccharomyces cerevisiae* APS kinase (found in Figure 2 of MacRae; GI 3529).

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<sup>1</sup> Although MacRae has a publication date after the earliest filing date of the instant application, Applicants submit that MacRae represents the state of knowledge of one of ordinary skill in the art, as of the earliest filing date of the instant application, at least with respect to the active site P-loop and (P)APS motifs associated with APS kinase activity, since these same motifs are disclosed in Satishchandran and Arz, which have publication dates well before the earliest filing date of the instant application.

<sup>2</sup> Applicants believe SEQ ID NO:14 to contain a transit peptide, based on the disclosure in Arz at page 450 of a transit peptide in an *Arabidopsis thaliana* APS kinase separated by a VRACVS sequence from the core protein (in Appendix A attached hereto, see amino acids 35-40 of GI 1076283). Applicants believe that SEQ ID NO:4 of the instant claims contains at least a part of a transit peptide on the N-terminus.

The active site P-loop and binding (P)APS motif in these four sequences are identified on Appendix A by boxes and are highly conserved in all four sequences.

In view of the foregoing, withdrawal of the Section 101 (utility) rejection is respectfully requested.

Regarding the Section 112, 1<sup>st</sup> paragraph rejection that one skilled in the art would not know how to use the claimed invention, the above remarks with respect to the Section 101 (utility rejection) apply here. Applicants respectfully traverse and request withdrawal of this rejection.

Regarding the Section 112, 1<sup>st</sup> paragraph written description rejection, Applicants respectfully traverse.

As an initial matter, Applicants submit that SEQ ID NO:3 is not a partial sequence as stated at the bottom of page 8 of the Office Action. As stated above, Applicants believe SEQ ID NO:3 to contain a single open reading frame of 1028 bp (from 2-1030) encoding a functionally complete protein of 343 amino acids (SEQ ID NO:4).

Under the PTO Written Description Guidelines, the written description requirement is met with disclosure of "functional characteristics when coupled with a known or disclosed correlation between function and structure." Guidelines, 66 Fed. Reg. at 1106.

Applicants submit that there is a well-known correlation between the APS kinase activity disclosed and claimed in the instant specification and APS kinase protein (and corresponding nucleic acid) structure, based on the remarks above with respect to Deyrup, Satishchandran, Arz, and MacRae and the active site P-loop and (P)APS motifs.

Given this known correlation between APS kinase activity and protein structure, Applicants submit that one of ordinary skill would readily recognize where amino acid substitutions could be made to result in a polypeptide sequence having 80% sequence identity to SEQ ID NO:4 while still retaining APS kinase activity.

Thus, the combination of the Applicants' disclosure and the known correlation of function and amino acid sequence structure renders the claims in compliance with the written description requirement.

For these reasons, Applicants respectfully request reconsideration and withdrawal of the Section 112, 1<sup>st</sup> paragraph

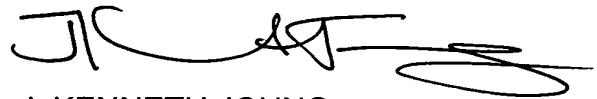
Regarding the Section 102(b) rejection over Arz, Applicants have Amended "complement" of Claim 12(b) to read "full-length complement." Withdrawal of the rejection is respectfully requested.

Applicants believe that the foregoing is responsive to each of the points recited in the Office Action, and submit that the present application is in allowable form. Favorable consideration and passage to issue are solicited.

The Commissioner is authorized to charge Deposit Account No. 04-1928 (E. I. du Pont de Nemours and Company) for any requisite fees due or to credit any overpayment.

Applicants' undersigned may be reached at the below-listed numbers.

Respectfully submitted,

A handwritten signature in black ink, appearing to read 'J. Kenneth JounG', with a long horizontal flourish extending to the right.

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Dated: 30 June 2003



# Appendix A

Consensus #1

.....  
10 20 30 40 50 60  
1 RPFHFINQTEPLVTHTQQPPSPAPGPASQ-GQRQGNLTLLSPPTTLAVILVNPQRAPPVLP BB1167B SEQIDN04  
1 ---MI GSVKRPVVSCVLPPEFDFTSTGLGKKSSSVKLPVNF---AFG GI 2832300  
1 ---MI AAGAKSLL-----GLSMA SPK-----IFD GI 1076283  
1 MA----- GI 3529

Consensus #1

.....  
70 80 90 100 110 120  
60 GLTPSDAPLPALVIHGLTPRSSHSSAGLASDSGRREGGRGARTHCHRGIGRWVRRRRN BB1167B SEQIDN04  
43 SGG--GEVKLGFLAPIKATEGSKTSS--FQVNGKVDNFRHLQPSDCNS-----NS GI 2832300  
23 SNMSNSRSRVVVRACVSM DGSQTLS--HNKNGSIPEVKSI----- GI 1076283  
3 ----- GI 3529

Consensus #1

.....  
130 140 150 160 170 180  
120 GAAPGEAPHSPVKEKPVMSNIGKSTNIIWHNCLIGQSDRQKLLGQKGCVVWITGLSGSGK BB1167B SEQIDN04  
89 DSSLNNCNGFPGKKILQTTTVGNSTNIIWHKCAVEKSERQEPHQQRGCVIWIITGLSGSGK GI 2832300  
62 -----NGHTGQKQGPLSTVGNSTNIKWHECSEVEKVDQRLLDQKGCVIWITGLSGSGK GI 1076283  
3 -----INITWHP-NLTYDERKALRKQDGGCTLWLTGLSASGK GI 3529

P-loop



P-loop continued

Consensus #1

STACAL...L...Y.LDGDN.R.GLN.DL.F...DR.ENIRR...EV.KLFAD...  
190 200 210 220 230 240  
STLACALSRGELHCRGHLTYVLDGDNLRHGLNRDLSEKAEEDRAENIRRVGGEVAKLFAADAGV  
STLACALSRGELHAKGKLTLYILDGDNVRRHGLNSDLSEKAEEDRAENIRRIIGEVAKLFAADAGV  
STLACALNQMLYQKGKLCYILDGDNVRRHGLNRDLSEKAEEDRAENIRRVGGEVAKLFAADAGI  
STLACALEQLLLQKNLSAYRRLDGDNIIRFGINKDLGESEKDRNENIRRISEVSKLFAADSCA

BB1167B SEQIDNO4  
GI 2832300  
GI 1076283  
GI 3529

Consensus #1

II.S.ISPYR...D...R.L...F.E.F.D.P.L...E.RDPKGLYK.A.R.G.I.K.F  
250 260 270 280 290 300  
ICIASLISPYRRDRDACRALLPHSN--FIEVFIDLPKICEARDPKGLYKILARTGKIKGF  
ICIASLISPYRKPPDACRSLLPEDD--FIEVFMDVPLKVCEARDPKGLYKILARAGKIKGF  
ICIASLISPYRTDRDACRSLLPEDD--FIEVFMDVPLSVCEARDPKGLYKILARAGKIKGF  
ISLTSFISPYRVDRDRARELHKEAGLKFEIIFVDVPLEVAEQORDPKGLYKILAREGVIKGF

BB1167B SEQIDNO4  
GI 2832300  
GI 1076283  
GI 3529

Consensus #1

TGI...PYE.P...E...Y.L...  
310 320 330 340 350  
TGIIDDPYEPPINGEIVIK--MKDEECPSPKAMAKQVLCYLEENGYLQA  
TGIIDDPYEPPINKSEIVLH--QKLGMDSPCDLADVISYLEENGYLKA  
TGIIDDPYEPPINCESISLG--REGG--TSPIEMAEKVVGYLDNKGYLQA  
TGISAPYEAPKAPELHLRTDQKTVEECAT-----TIYEVLISEKIIIRKHL

BB1167B SEQIDNO4  
GI 2832300  
GI 1076283  
GI 3529

Consensus 'Consensus #1': When all match the residue of the Consensus show the residue of the Consensus, otherwise show '.'.

Decoration 'Decoration #1': Shade (with black at 40% fill) residues that match the Consensus exactly.